WHAT IS CLAIMED IS:

1. A substantially pure or isolated polypeptide comprising a segment exhibiting sequence homology to a corresponding portion of a mature protein selected from the group consisting of:

i) TECK;

ii) MIP-3α;

iii) MIP-3β;

iv) DC CR; and

v) M/DC CR;

wherein said homology is at least about 70% identity and said portion is at least about 25 amino acids.

2. The protein of Claim 1, further comprising a second segment exhibiting:

a) at least about 90% identity over at least 9 amino acids; or

b) at least about 80% identity over at least 17 amino acids.

3. The polypeptide of Claim 1, wherein said polypeptide:

a) is from a warm blooded animal selected from the group of birds and mammals, including a mouse or human;

b) comprises a natural sequence from Tables 1 through 5;

c) exhibits a post-translational modification pattern distinct from a natural form of said polypeptide;

d) is made by expression of a recombinant nucleic acid;

e) comprises synthetic sequence;

f) is detectably labeled;

g) is conjugated to a solid substrate;

h) is conjugated to another chemical moiety;

i) is a fusion protein;

j) is in a denatured conformation, including detergent denaturation;
k) further comprises an epitope tag;
l) is an immunogenic polypeptide;
m) has a defined homogeneous molecular weight;
n) is useful as a carbon source;
o) is an allelic variant of SEQ ID NO: 2, 4, 6, 8, 10, or 12;
p) is a 3-fold or less substituted form of a natural sequence;
q) is in a sterile composition;
r) is in a buffered solution or suspension;
s) is in a regulated release device;
t) comprises a post-translational modification;
u) is in a cell; or
v) is in a kit which further comprises instructions for use or disposal of reagents therein.

4. An isolated or recombinant nucleic acid encoding said protein of Claim 1, where said portion consists of sequence from the coding region of SEQ ID NO: 1, 3, 5, 7, 9, or 11.

5. The nucleic acid of Claim 4, wherein said nucleic acid:
a) exhibits at least about 80% identity to a natural cDNA encoding said segment;
b) is in an expression vector;
c) further comprises a promoter;
d) further comprises an origin of replication;
e) is from a natural source;
f) is detectably labeled;
g) comprises synthetic nucleotide sequence;
h) is less than 6 kb;
i) is from a mammal;
j) comprises a natural full length mature coding sequence;

k) is in a kit, which also comprises instructions for use or disposal of reagents therein;

l) is a specific hybridization probe for a gene encoding said protein;

m) is a PCR product; or

n) is in a cell.

6. A method of using a purified nucleic acid of Claim 5, comprising a step of expressing said nucleic acid to produce a protein.

7. An isolated or recombinant nucleic acid which encodes at least eight consecutive residues of SEQ ID NO: 2, 4, 6, 8, 10, or 12.

8. The nucleic acid of Claim 7, which encodes at least:

a) twelve consecutive residues from SEQ ID NO: 2, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 1;

b) twelve consecutive residues from SEQ ID NO: 4, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 3;

c) twelve consecutive residues from SEQ ID NO: 6, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 5;

d) twelve consecutive residues from SEQ ID NO: 8, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 7;

e) twelve consecutive residues from SEQ ID NO: 10, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 9; or

f) twelve consecutive residues from SEQ ID NO: 12, and further comprises a coding sequence of at least 17 nucleotides from SEQ ID NO: 11.

9. The nucleic acid of Claim 7, wherein said nucleic acid:

a) exhibits at least about 80% identity to a natural cDNA encoding said segment;
b) is in an expression vector;
c) further comprises a promoter;
d) further comprises an origin of replication;
e) encodes a 3-fold or less substituted sequence from a natural sequence;
f) is from a natural source;
g) is detectably labeled;
h) comprises synthetic nucleotide sequence;
i) is less than 6 kb;
j) is from a mammal;
k) is attached to a solid substrate, including in a Southern or Northern blot;
l) comprises a natural full length coding sequence;
m) is in a cell; or
n) is in a detection kit, which also comprises instructions for use or disposal of reagents therein.

10. A nucleic acid which hybridizes under stringent wash conditions of 55° C and less than 150 mM salt to the nucleic acid of Claim 7.

11. The nucleic acid of Claim 10, which exhibits at least about 85% identity over a stretch of at least about 30 nucleotides to a primate sequence of SEQ ID NO: 1, 3, 5, 7, 9, or 11.

12. The nucleic acid of Claim 10, wherein:

a) said identity is at least 90%; or
b) said stretch is at least 75 nucleotides.

13. The nucleic acid of Claim 10, wherein:

a) said identity is at least 95%; or

b) said stretch is at least 100 nucleotides.

14. A binding compound comprising an antigen binding fragment from an antibody which binds to a protein of Claim 1.

15. The binding compound of Claim 14, wherein:

a) said polypeptide is a mouse or human protein;
b) said antibody is raised against a mature peptide sequence of Tables 1 through 5;
c) said antibody is a monoclonal antibody;
d) said binding compound is attached to a solid substrate;
e) said binding compound is in a sterile composition;
f) said binding compound binds to a denatured antigen, including a detergent denatured antigen;
g) said binding compound is detectably labeled;
h) said binding compound is an Fv, Fab, or Fab2 fragment;
i) said binding compound is conjugated to a chemical moiety;
j) said binding compound is in a detection kit which also comprises instructions for use or disposal of reagents therein.

16. A cell which makes said antibody of Claim 14.

17. A method of purifying a polypeptide using a binding compound of Claim 14 to specifically separate said polypeptides from others.

18. A method of generating an antigen-binding compound complex comprising the step of contacting a sample comprising said antigen to a sample comprising a binding compound of Claim 14.

19. A method of modulating physiology or development of a cell expressing a receptor for a chemokine selected from the group selected from:

a) TECK;

b) MIP-3α; or

c) MIP-3β;

comprising contacting said cell with a composition comprising:

i) an agonist or mutein of said chemokine; or

ii) an antibody antagonist of said chemokine.

20. The method of Claim 19, wherein said cell is a macrophage or lymphocyte.

21. The method of Claim 19, wherein said physiology is selected from:

a) a cellular calcium flux;

b) a chemoattractant response;

c) cellular morphology modification responses;

d) phosphoinositide lipid turnover; or

e) an antiviral response.

22. The method of Claim 19, wherein:

a) said receptor is DC CR and said chemokine is MIP-3α;

b) said physiology is pulmonary physiology; or

c) said cell is an eosinophil.

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